SEQUENCE LISTING

<110> Guenther, Catherine
     Allen, Keith D.

<120> TRANSGENIC MICE CONTAINING NOR1 GENE
   DISRUPTIONS

<130> R-687

<150> US 60/251,794
<151> 2000-12-06

<150> US 60/324,614
<151> 2001-09-24

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1884
<212> DNA
<213> Mus musculus

<400> 1
atgccctgcg tgcaagccca gtatagccct tcacctccgg ggtccactta cgccacgcag 60
acttatggct cggaatacac cacagaaatc atgaaccccg actacaccaa gctgaccatg 120
gacctcggta gcacggggat catggccacc gccactacat ccctgcccag cttcagtacc 180
ttcatggagg gctaccccag cagctgcgaa ctcaagccct cctgcctgta ccaaatgccg 240
cctttctgggc ctcggccttt gatcaagatg gaagagggtc gcgagcatgg ctaccaccac 300
caccatcacc atcaccatca tcaccaccac caccagcaac agcagccgtc cattcctcct 360
ccctccggcc ccgaggacga ggtactgccc agcacctcca tgtacttcaa gcagtctccg 420
ccgtctacac cgaccactcc aggcttcccc ccgcaggcgg gggcgctgtg ggacgacgag 480
ctgccctctg cgcctggctg catcgctccg ggaccgctgc tggacccgca gatgaaggcg 540
gtacccccaa tggccgctgc tgcgcgcttc ccgatcttct tcaagccctc accgccacac 600
cctcccgcgc ccagtccagc cggcggccac cacctcggct atgaccccac ggccgcagct 660
gcactcagtc tgccccctggg agccgcggcc gcagcaggca gccaagctgc tgcgctcgag 720
ggccacccat acgggctccc gctggccaag aggacggcca cgctgacctt ccctccgctg 780
ggcctcacag cctcccccac cgcgtccagc ctgctgggag agagccccag cctcccatcg 840
ccacccaata ggagctcatc atctggggaa ggcacatgtg ccgtgtgcgg cgacaacgct 900
gcctgccagc actacggagt ccgcacctgc gagggctgca agggcttctt caagagaacg 960
gtgcagaaaa atgcaaaata tgtttgcctg gcaaataaaa actgcccagt ggacaagaga 1020
cgccgaaacc gatgtcagta ctgcagattt cagaagtgtc tcagtgtcgg gatggttaag 1080
gaagttgtgc gtacagacag tctgaaaggg aggagaggtc gtctgccttc caaaccaaag 1140
agcccactac aacaggagcc ctcgcagccc tccccgccat ctcctccgat ctgtatgatg 1200
aatgcccttg tccgagcttt aacagatgca acacccagag atcttgatta ttccagatac 1260
tgtcccaccg accaggccac tgcaggcaca gatgctgagc acgtgcaaca gttctacaac 1320
cttctgacgg cctccattga cgtgtccaga agctgggcag aaaagatccc aggattcact 1380
gatctcccca aagaagatca gacgttactt atagaatcag ccttttttgga gctgtttgtt 1440
cttagacttt ccatcaggtc aaacactgct gaagataagt ttgtgttctg caatggactt 1500
gtcctgcatc gacttcagtg ccttcgagga tttgggggagt ggctcgactc cattaaagac 1560
ttttctttaa acttgcagag cctgaaccct gatatccaag ccttagcctg ggctgtcagca 1620
ctgagtatga tcacagagcg acatgggtta aaagaaccaa agagagtgga ggagctatgc 1680
accaagatca caagcagctt aaaggaccac cagaggaagg gacaggctct ggagccctcg 1740
gagcctaagg tcctgcgcgc gctggtagaa ctgagaaaga tctgtacccca gggcctccag 1800
cgcatcttct acctgaagct agaggacttg gtacctccac cttctgtcat cgacaagctc 1860
ttccttgaca ccctgccttt ctga 1884

<210> 2

1

<211> 627
<212> PRT
<213> Mus musculus

<400> 2

```
Met Pro Cys Val Gln Ala Gln Tyr Ser Pro Ser Pro Pro Gly Ser Thr
1               5                   10                  15
Tyr Ala Thr Gln Thr Tyr Gly Ser Glu Tyr Thr Thr Glu Ile Met Asn
                20                  25                  30
Pro Asp Tyr Thr Lys Leu Thr Met Asp Leu Gly Ser Thr Gly Ile Met
        35                  40                  45
Ala Thr Ala Thr Thr Ser Leu Pro Ser Phe Ser Thr Phe Met Glu Gly
    50                  55                  60
Tyr Pro Ser Ser Cys Glu Leu Lys Pro Ser Cys Leu Tyr Gln Met Pro
65                  70                  75                  80
Pro Ser Gly Pro Arg Pro Leu Ile Lys Met Glu Glu Gly Arg Glu His
                85                  90                  95
Gly Tyr His His His His His His His His His His His His His Gln
            100                 105                 110
Gln Gln Gln Pro Ser Ile Pro Pro Pro Ser Gly Pro Glu Asp Glu Val
        115                 120                 125
Leu Pro Ser Thr Ser Met Tyr Phe Lys Gln Ser Pro Pro Ser Thr Pro
    130                 135                 140
Thr Thr Pro Gly Phe Pro Pro Gln Ala Gly Ala Leu Trp Asp Asp Glu
145                 150                 155                 160
Leu Pro Ser Ala Pro Gly Cys Ile Ala Pro Gly Pro Leu Leu Asp Pro
                165                 170                 175
Gln Met Lys Ala Val Pro Pro Met Ala Ala Ala Ala Arg Phe Pro Ile
            180                 185                 190
Phe Phe Lys Pro Ser Pro Pro His Pro Pro Ala Pro Ser Pro Ala Gly
        195                 200                 205
Gly His His Leu Gly Tyr Asp Pro Thr Ala Ala Ala Ala Leu Ser Leu
    210                 215                 220
Pro Leu Gly Ala Ala Ala Ala Ala Gly Ser Gln Ala Ala Ala Leu Glu
225                 230                 235                 240
Gly His Pro Tyr Gly Leu Pro Leu Ala Arg Thr Ala Thr Leu Thr
                245                 250                 255
Phe Pro Pro Leu Gly Leu Thr Ala Ser Pro Thr Ala Ser Ser Leu Leu
        260                 265                 270
Gly Glu Ser Pro Ser Leu Pro Ser Pro Pro Asn Arg Ser Ser Ser Ser
    275                 280                 285
Gly Glu Gly Thr Cys Ala Val Cys Gly Asp Asn Ala Ala Cys Gln His
    290                 295                 300
Tyr Gly Val Arg Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr
305                 310                 315                 320
Val Gln Lys Asn Ala Lys Tyr Val Cys Leu Ala Asn Lys Asn Cys Pro
                325                 330                 335
Val Asp Lys Arg Arg Arg Asn Arg Cys Gln Tyr Cys Arg Phe Gln Lys
            340                 345                 350
Cys Leu Ser Val Gly Met Val Lys Glu Val Val Arg Thr Asp Ser Leu
        355                 360                 365
Lys Gly Arg Arg Gly Arg Leu Pro Ser Lys Pro Lys Ser Pro Leu Gln
    370                 375                 380
Gln Glu Pro Ser Gln Pro Ser Pro Pro Ser Pro Pro Ile Cys Met Met
385                 390                 395                 400
Asn Ala Leu Val Arg Ala Leu Thr Asp Ala Thr Pro Arg Asp Leu Asp
                405                 410                 415
Tyr Ser Arg Tyr Cys Pro Thr Asp Gln Ala Thr Ala Gly Thr Asp Ala
            420                 425                 430
Glu His Val Gln Gln Phe Tyr Asn Leu Leu Thr Ala Ser Ile Asp Val
        435                 440                 445
```

2

```
Ser Arg Ser Trp Ala Glu Lys Ile Pro Gly Phe Thr Asp Leu Pro Lys
    450                 455                 460
Glu Asp Gln Thr Leu Leu Ile Glu Ser Ala Phe Leu Glu Leu Phe Val
465                 470                 475                 480
Leu Arg Leu Ser Ile Arg Ser Asn Thr Ala Glu Asp Lys Phe Val Phe
                485                 490                 495
Cys Asn Gly Leu Val Leu His Arg Leu Gln Cys Leu Arg Gly Phe Gly
                500                 505                 510
Glu Trp Leu Asp Ser Ile Lys Asp Phe Ser Leu Asn Leu Gln Ser Leu
            515                 520                 525
Asn Leu Asp Ile Gln Ala Leu Ala Cys Leu Ser Ala Leu Ser Met Ile
        530                 535                 540
Thr Glu Arg His Gly Leu Lys Glu Pro Lys Arg Val Glu Glu Leu Cys
545                 550                 555                 560
Thr Lys Ile Thr Ser Ser Leu Lys Asp His Gln Arg Lys Gly Gln Ala
                565                 570                 575
Leu Glu Pro Ser Glu Pro Lys Val Leu Arg Ala Leu Val Glu Leu Arg
                580                 585                 590
Lys Ile Cys Thr Gln Gly Leu Gln Arg Ile Phe Tyr Leu Lys Leu Glu
        595                 600                 605
Asp Leu Val Pro Pro Ser Val Ile Asp Lys Leu Phe Leu Asp Thr
    610                 615                 620
Leu Pro Phe
625


<210> 3
<211> 4400
<212> DNA
<213> ratus norvegius

<400> 3
ccgagtctcc tgcctcccgc cccccacccc tccagcgcct gctcctcctc cgctccccat 60
acacagacac gctcacaccc gctccttcac ttgcacacac agacacacgc gcgctcacac 120
gctccgcaca cacactccac tctctcccgc gcgctcacac ccctctctct cggcgccctc 180
gccggtgtcg cgccgcgccg cgccgcagcc ggacgccct ccaggggctca ctttgcaacg 240
ctgacagagc gggagctggc cgtggaggtg ggaaacgtgg cgacatccta gcccctggcc 300
gcagccggag actggacgct gcggaacctc tcggcggcgc tctcccatga gttgggggatcg 360
cagcatcccc aggcagccgc tgctcaccgc ctctgggagc cgctgggttt gtgcaccgca 420
gcccttccgg gacagcagct gtgactctcc cccaatccag atttcggggt cgctctctag 480
aaactcgctc taaagacgga acctccacag aacccaaagc ccactgcggg agagcgcagc 540
ccgacaagcc cgggcgctga gcctggaccc tcaacagagc gggccagcac agcggcggcg 600
gctgcttcgc ctatcccgac gtccccgcct cctacatct cagcctccgc tggagagacc 660
cccagccca ccattcagcg cgcaagatac cctccagata tgccctgcgt gcaagcccaa 720
tatagccctt cgcctccggg gtccacttat gccacgcaga cttatggctc ggaatacacc 780
acagaaatca tgaacccca ctatgccaag ctgaccatgg acctcggtag cacggggatc 840
atggccacgg ccacgacgtc cctgcccagc ttcagtacct tcatggaggg ctaccccagc 900
agctgcgaac tcaagccctc ctgcctgtac caaatgccgc cttctggcc tcggcctttg 960
atcaagatgg aagagggtcg cgagcatggc taccaccacc accaccacca tcaccatcat 1020
catcaccacc accaccagca gcagcagccg tccattcctc ctccctctgg cccggaggac 1080
gaggtactgc ccagcacctc catgtacttc aagcagtctc cgccgtctac gccgaccact 1140
ccaggcttcc ccccgcaggc ggggcgctg tgggacgacg agctgccctc tgggaatacacc 1200
tgcatcgctc cgggaccgct gctggacccg cagatgaagg cagtgccccc aatggccgct 1260
gctgcgcgct tcccgatctt cttcaagccc tcaccgccac acctccccgc gcccagccca 1320
gccggcggcc accacctggg ctatgaccc acggccgcag ctgcgctcag tctacccctg 1380
ggagccgggg ccgccgcggg cagccaagct gctgcgctcg agggccatcc gtacgggctc 1440
ccgctggcca agaggacggc cacgttgacc ttccctccgc tgggcctcac agcgtcccct 1500
accgcgtcca gcctgctggg agagagcccc agcctaccat cgcacacccaa taggagctca 1560
tcatccggcg agggcacgtg tgctgtgtgc agacgcaatg ctgcctgcca gcactacgga 1620
gtccgcacct gcgagggctg caagggcttc ttcaagagaa cggtgcagaa aaacgcaaaa 1680
tatgtttgct tggcaaataa aaactgcccg gtagacaaga gacgtcgaaa tcgatgtcag 1740
```

```
tactgcaggt ttcagaagtg tctcagtgtc gggatggtga aggaagttgt gcgtacagat 1800
agtctgaaag ggaggagagg tcgtctgcct tccaaaccaa agagcccact acaacaggag 1860
ccctcgcagc cctccccacc atctcctccg atctgtatga tgaacgccct tgtccgagct 1920
ttaacagacg caacgcccag agaccttgat tactccagat actgtcccac cgaccaggcc 1980
actgcgggca cagacgctga gcacgtgcag cagttctaca accttctgac ggcctccatc 2040
gacgtgtcca gaagctgggc agaaaagatc cccggattca ctgatctccc caaagaagat 2100
cagacgttac ttatagaatc agcctttttg gagctgttcg tcttagact ttctatcagg 2160
tcaaacactg ctgaagataa gtttgtgttc tgcaatggac ttgtcctgca ccgacttcag 2220
tgccttcgcg gatttgggga gtggctcgac tccattaaag acttttcttt aaatttgcag 2280
agcctgaacc ttgatatcca agccttagcc tgcctgtcag cactgagtat gatcacagag 2340
cgacatgggt taaaagaacc aaagagagtg gaggagctat gcaacaagat cacaagcagc 2400
ttaaaggacc accagaggaa gggacaggct ctggagccct cagagcccaa ggtccttcgt 2460
gcactggtgg aactgaggaa gatctgcacc cagggcctcc agcgtatctt ctacctgaag 2520
ctggaggact tggtgtcccc accttctgtc atcgacaagc tcttccttga taccctgcct 2580
ttctgagcag gggaagcctg agcagagagc tacttgctct gctggcactg gtcattaagt 2640
gagcaaaagg atgggtttga acacctgccc ctctatcctt cctccagggg aaaaagcagt 2700
tcccatagaa agcaaagact ttttttttc ctggcacctt tccttacaac ctaaagccag 2760
aaaccttgca gagtattgtg ttggggttgt gtttttatatt taggctttgg tgggtgggct 2820
gggaggggt aaaatagttc atgaggcttt tctaagaaat tgctgacgaa gcacttttgg 2880
atgatgctat cccagcagtg gggtgggag aaaggataat ataactgttt taaaaactct 2940
ttccggggga atatgactat ggttgctttg tatttaaaaa taagaacagc caagggctgt 3000
tttaccaggg tagggctgtg tcttaagact gatcccttta gtatgtactt cccggatcga 3060
ggcacataag tggtgcaaat gaggcgggga aattcttcat ttcttcattt cttcttctt 3120
cttaaaataa aatggcaaaa aaaaaaagat ggaagattat ctacaaatca gacttagcaa 3180
aatgataatg tgcttcgct tccacataca agtgcaattt tttagagtgc tgtcttacta 3240
agtcttgttt gtgaactctc cctcatttta tatgaaaata agaaggaggc agtcatgtta 3300
tcaaacgcg tgctcatttt cctagctcac cctggtccaa cctgcccgt agaaccccttc 3360
ggaggtatgg cccttctaag acttttcaggc cactcttgat ggaattcgac accctcccc 3420
tcaacccatg actatccaga tgtcctgaat ggggatcagg ttataaaatg gattgcatat 3480
gactgtgttc gctgtgtgtt tgtcaacctg gacagagttc tctaaacctt ctttagttgt 3540
agcaagttcc tgattcctcc attcagaagc ccaaggagca ttgggtgact cgatcaaggg 3600
ttaaccctag gagaacatgc aaataagtag gaactgggtc agacagggta agcaccagag 3660
atgataagga tttatatata aatatatata aaattaattt tgttattggg ttatagacaa 3720
ttttggaaag caagagaatc atctctttt ttttttttaaa gaggaaaaga tagtattgat 3780
gtattagcaa agattagtgg ggtacggttc aacattccgt gtttgtgccc ccttttctat 3840
gtttctactg ttgatggcat attattataga aatgattcgt tgcatagtgt ccttatttgt 3900
atgaacattt gtatgcacgt tctattgtaa tcgctttgcc tgtatttatt gcaagaccac 3960
cagctcctgg aggctgagtt acagaataat caaatggggt gttcgtggtg acttggatac 4020
accggttaga aattaaataa gcatatatat atatataaaa acatagcagg ttacatatat 4080
atttataatg tgtcttttta ttaaccattt gtacaataaa tgtcacttcc cacgcagtta 4140
ttttatcctt tgttttgcagt gacctttaag gcagcactgt ttagcacttt gatatgaaat 4200
tttttgctta ttttttttgct aaattcaaat aacgtttgaa gattttttagg tctaaaagtc 4260
tttatattat atacactgta tcaagtcaag atacctttgg ccgttttgct aagactcaaa 4320
ctttgaatgt caaaccaatg tcacggtagc ttctgttagc tttaatcat ttttgcttta 4380
gtcttttttt ttaaaaaaaaa 4400

<210> 4
<211> 628
<212> PRT
<213> Ratus norvegius

<400> 4
Met Pro Cys Val Gln Ala Gln Tyr Ser Pro Ser Pro Pro Gly Ser Thr
1               5                   10                  15
Tyr Ala Thr Gln Thr Tyr Gly Ser Glu Tyr Thr Thr Glu Ile Met Asn
            20                  25                  30
Pro Asp Tyr Ala Lys Leu Thr Met Asp Leu Gly Ser Thr Gly Ile Met
        35                  40                  45
Ala Thr Ala Thr Thr Ser Leu Pro Ser Phe Ser Thr Phe Met Glu Gly
    50                  55                  60
Tyr Pro Ser Ser Cys Glu Leu Lys Pro Ser Cys Leu Tyr Gln Met Pro
```

4

```
65                    70                    75                    80
Pro Ser Gly Pro Arg Pro Leu Ile Lys Met Glu Glu Gly Arg Glu His
                    85                    90                    95
Gly Tyr His His His His His His His His His His His His His His
          100                   105                   110
Gln Gln Gln Gln Pro Ser Ile Pro Pro Pro Ser Gly Pro Glu Asp Glu
          115                   120                   125
Val Leu Pro Ser Thr Ser Met Tyr Phe Lys Gln Ser Pro Pro Ser Thr
      130                   135                   140
Pro Thr Thr Pro Gly Phe Pro Pro Gln Ala Gly Ala Leu Trp Asp Asp
145                   150                   155                   160
Glu Leu Pro Ser Ala Pro Gly Cys Ile Ala Pro Gly Pro Leu Leu Asp
                  165                   170                   175
Pro Gln Met Lys Ala Val Pro Pro Met Ala Ala Ala Ala Arg Phe Pro
              180                   185                   190
Ile Phe Phe Lys Pro Ser Pro Pro His Pro Pro Ala Pro Ser Pro Ala
          195                   200                   205
Gly Gly His His Leu Gly Tyr Asp Pro Thr Ala Ala Ala Ala Leu Ser
      210                   215                   220
Leu Pro Leu Gly Ala Ala Ala Ala Ala Gly Ser Gln Ala Ala Ala Leu
225                   230                   235                   240
Glu Gly His Pro Tyr Gly Leu Pro Leu Ala Lys Arg Thr Ala Thr Leu
                  245                   250                   255
Thr Phe Pro Pro Leu Gly Leu Thr Ala Ser Pro Thr Ala Ser Ser Leu
              260                   265                   270
Leu Gly Glu Ser Pro Ser Leu Pro Ser Pro Pro Asn Arg Ser Ser Ser
      275                   280                   285
Ser Gly Glu Gly Thr Cys Ala Val Cys Gly Asp Asn Ala Ala Cys Gln
290                   295                   300
His Tyr Gly Val Arg Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg
305                   310                   315                   320
Thr Val Gln Lys Asn Ala Lys Tyr Val Cys Leu Ala Asn Lys Asn Cys
                  325                   330                   335
Pro Val Asp Lys Arg Arg Arg Asn Arg Cys Gln Tyr Cys Arg Phe Gln
              340                   345                   350
Lys Cys Leu Ser Val Gly Met Val Lys Glu Val Val Arg Thr Asp Ser
      355                   360                   365
Leu Lys Gly Arg Arg Gly Arg Leu Pro Ser Lys Pro Lys Ser Pro Leu
      370                   375                   380
Gln Gln Glu Pro Ser Gln Pro Ser Pro Pro Ser Pro Pro Ile Cys Met
385                   390                   395                   400
Met Asn Ala Leu Val Arg Ala Leu Thr Asp Ala Thr Pro Arg Asp Leu
                  405                   410                   415
Asp Tyr Ser Arg Tyr Cys Pro Thr Asp Gln Ala Thr Ala Gly Thr Asp
          420                   425                   430
Ala Glu His Val Gln Gln Phe Tyr Asn Leu Leu Thr Ala Ser Ile Asp
      435                   440                   445
Val Ser Arg Ser Trp Ala Glu Lys Ile Pro Gly Phe Thr Asp Leu Pro
      450                   455                   460
Lys Glu Asp Gln Thr Leu Leu Ile Glu Ser Ala Phe Leu Glu Leu Phe
465                   470                   475                   480
Val Leu Arg Leu Ser Ile Arg Ser Asn Thr Ala Glu Asp Lys Phe Val
              485                   490                   495
Phe Cys Asn Gly Leu Val Leu His Arg Leu Gln Cys Leu Arg Gly Phe
          500                   505                   510
Gly Glu Trp Leu Asp Ser Ile Lys Asp Phe Ser Leu Asn Leu Gln Ser
      515                   520                   525
Leu Asn Leu Asp Ile Gln Ala Leu Ala Cys Leu Ser Ala Leu Ser Met
      530                   535                   540
Ile Thr Glu Arg His Gly Leu Lys Glu Pro Lys Arg Val Glu Glu Leu
545                   550                   555                   560
```

5

```
Cys Asn Lys Ile Thr Ser Ser Leu Lys Asp His Gln Arg Lys Gly Gln
                565                     570                 575
Ala Leu Glu Pro Ser Glu Pro Lys Val Leu Arg Ala Leu Val Glu Leu
            580                     585                 590
Arg Lys Ile Cys Thr Gln Gly Leu Gln Arg Ile Phe Tyr Leu Lys Leu
        595                     600                 605
Glu Asp Leu Val Ser Pro Pro Ser Val Ile Asp Lys Leu Phe Leu Asp
    610                     615                 620
Thr Leu Pro Phe
625


<210> 5
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Targeting Vector

<400> 5
cccctttgaca gtcaggaact cagctgtctt cccagccagg aagaaagtaa gctaggagca    60
ttcagtcttt gccagcaggt gggagaggat accactttct tgtttcctga ttcaagagca   120
gtggaaccag ctgcagatgg agtgtcaact ggcttctgag ccctttctc tgtccctcca    180
gatatgccct gcgtgcaagc                                               200


<210> 6
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Targeting Vector

<400> 6
ctttgatcaa gatggaagag gatcgcgagc atggctacca ccaccaccat caccatcacc    60
atcatcacca ccaccaccag caacagcagc cgtccattcc tcctccctcc ggccccgagg   120
acgaggtact gcccagcacc tccatgtact tcaagcagtc tccgccgtct acaccgacca   180
ccccaggctt ccccccgcag                                               200
```